

U.S. Application Serial
No. 09/333,159

Attorney Docket No.
MBI099-030RCEM

**Marked Up Copy of Claims, as Amended
in the Amendment Filed in Response to the
Office Action Dated February 14, 2003**

1. (Amended Four Times) An isolated nucleic acid molecule, or its complement, wherein the isolated nucleic acid i) encodes a polypeptide which exhibits lipase activity and ii) is selected from the group consisting of:

a) a nucleic acid molecule having a nucleotide sequence which is at least 90% identical to the nucleotide sequence of SEQ ID NO: 45 or 46;

b) a nucleic acid molecule comprising a fragment of SEQ ID NO: 45 or 46;

c) a nucleic acid molecule which encodes a polypeptide comprising the amino acid sequence encoded by SEQ ID NO: 46;

d) a nucleic acid molecule which encodes a fragment of the amino acid sequence encoded by SEQ ID NO: 46; and

e) a nucleic acid molecule which encodes a variant of the amino acid sequence encoded by SEQ ID NO: 46, wherein the nucleic acid molecule hybridizes over its full length in 6× sodium chloride/sodium citrate (SSC) at about 45°C, followed by one or more washes in 0.2× SSC, 0.1% SDS at 50°C with a portion of a nucleic acid molecule consisting of the nucleotide sequence of SEQ ID NO: 45 or 46.

39. (Twice Amended) The isolated nucleic acid molecule of claim 1, or its complement, wherein the molecule hybridizes over its full length in 6× SSC at about 45°C, followed by one or more washes in 0.2× SSC, 0.1% SDS at 50°C with a nucleic acid molecule consisting of the nucleotide sequence of SEQ ID NO: 45 or 46.

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33. (Twice Amended) The isolated nucleic acid molecule of claim 30, or its complement, wherein the nucleic acid molecule encodes a polypeptide comprising a fragment which comprises consecutive amino acid residues ~~comprise~~ an immunogenic portion of the protein having the amino acid sequence encoded by SEQ ID NO: 46.

32. (Thrice Amended) The isolated nucleic acid molecule of claim 1, or its complement, wherein the nucleic acid molecule encodes a variant of the amino acid sequence encoded by SEQ ID NO: 46, wherein the nucleic acid molecule hybridizes over its full length in 6× SSC at about 45°C, followed by one or more washes in 0.2× SSC, 0.1% SDS at 50°C with a nucleic acid molecule consisting of the nucleotide sequence of SEQ ID NO: 45 or 46.

37. (Thrice Amended) The method of claim 12, wherein the polypeptide is a variant of the polypeptide encoded by SEQ ID NO: 46, wherein the polypeptide is encoded by a nucleic acid molecule which hybridizes over its full length in 6× SSC at about 45°C, followed by one or more washes in 0.2× SSC, 0.1% SDS at 50°C with a nucleic acid molecule consisting of the nucleotide sequence of SEQ ID NO: 45 or 46, or a complement thereof.

43. (Amended) An isolated nucleic acid molecule, or its complement, wherein the isolated nucleic acid i) encodes an immunogenic portion of the protein having the amino acid sequence encoded by SEQ ID NO: 46 and ii) is selected from the group consisting of:

- a) a nucleic acid molecule having a nucleotide sequence which is at least 90% identical to the nucleotide sequence of SEQ ID NO: 45 or 46;
- b) a nucleic acid molecule comprising a fragment of SEQ ID NO: 45 or 46;
- c) a nucleic acid molecule which encodes a polypeptide comprising the amino acid sequence encoded by SEQ ID NO: 46;

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MBI099-030RCM


d) a nucleic acid molecule which encodes a fragment of the amino acid sequence encoded by SEQ ID NO: 46; and

e) a nucleic acid molecule which encodes a variant of the amino acid sequence encoded by SEQ ID NO: 46, wherein the nucleic acid molecule hybridizes over its full length in 6× sodium chloride/sodium citrate (SSC) at about 45°C, followed by one or more washes in 0.2× SSC, 0.1% SDS at 50°C with a portion of a nucleic acid molecule consisting of the nucleotide sequence of SEQ ID NO: 45 or 46.

44. (Amended) The isolated nucleic acid molecule of claim 43, or its complement, wherein the molecule hybridizes over its full length in 6× SSC at about 45°C, followed by one or more washes in 0.2× SSC, 0.1% SDS at 50°C with a nucleic acid molecule consisting of the nucleotide sequence of SEQ ID NO: 45 or 46.

54. (Amended) The isolated nucleic acid molecule of claim 43, or its complement, wherein the nucleic acid molecule encodes a variant of the amino acid sequence encoded by SEQ ID NO: 46, wherein the nucleic acid molecule hybridizes over its full length in 6× SSC at about 45°C, followed by one or more washes in 0.2× SSC, 0.1% SDS at 50°C with a nucleic acid molecule consisting of the nucleotide sequence of SEQ ID NO: 45 or 46.

65. (Twice Amended) The method of claim 62, wherein the immunogenic portion is from a polypeptide ~~is a~~ variant of the polypeptide encoded by SEQ ID NO: 46, wherein the polypeptide is encoded by a nucleic acid molecule which hybridizes over its full length in 6× SSC at about 45°C, followed by one or more washes in 0.2× SSC, 0.1% SDS at 50°C with a nucleic acid molecule consisting of the nucleotide sequence of SEQ ID NO: 45 or 46, or a complement thereof.

| | | | | |
|---|--------------------------|-------------------------------|----------------------------|-------------------------|
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| Hosted by NCSC US Mirror sites: Canada China Korea Switzerland Taiwan | | | | |
| Search <input type="text" value="PROSITE"/> for <input type="text"/> | | | | |

NiceSite View of PROSITE: PS00120

| General information about the entry | |
|--|---|
| Entry name | LIPASE_SER |
| Accession number | PS00120 |
| Entry type | PATTERN |
| Date | APR-1990 (CREATED); NOV-1997 (DATA UPDATE); JUL-1998 (INFO UPDATE). |
| PROSITE documentation | PDOC00110 |
| Name and characterization of the entry | |
| Description | Lipases, serine active site. |
| Pattern | [LIV]-x-[LIVFY]-[LIVMST]-G-[HYWV]-S-x-G-[GSTAC]. |
| Numerical results | |
| <ul style="list-style-type: none"> • SWISS-PROT release number: 40.7, total number of sequence entries in that release: 103373. • Total number of hits in SWISS-PROT: 113 hits in 113 different sequences • Number of hits on proteins that are known to belong to the set under consideration: 73 hits in 73 different sequences • Number of hits on proteins that could potentially belong to the set under consideration: 2 hits in 2 different sequences • Number of false hits (on unrelated proteins): 38 hits in 38 different sequences • Number of known missed hits: 10 • Number of partial sequences which belong to the set under consideration, but which are not hit by the pattern or profile because they are partial (fragment) sequences: 2 • Precision (true hits / (true hits + false positives)): 65.77 % • Recall (true hits / (true hits + false negatives)): 87.95 % | |
| Comments | |
| <ul style="list-style-type: none"> • Taxonomic range: Eukaryotes, Prokaryotes (Bacteria) • Maximum known number of repetitions of the pattern in a single protein: 1 • 'Interesting' site in the pattern: 7,active_site | |
| Cross-references | |
| <p>True positive hits:</p> <p>LCAT_CLEGL (Q35502), LCAT_HUMAN (P04180), LCAT_MOUSE (P16301), LCAT_PAPAN (Q08758), LCAT_RABIT (P53761), LCAT_RAT (P18424), LCAT_TATKG (Q35840), LICH_HUMAN (P38571), LIP1_CANFA (P06857), LIP1_HUMAN (P54315), LIP1_RAT (P54316), LIP2_HUMAN (P54317), LIP2_RAT (P54318), LIP3_DROME (O46108), LIP_BURCE (P22088), LIP_PSEAE (P26876), LIP_PSEFR (P08658), LIP_PSEGL (Q05489), LIP_PSES5 (P25275), LIP_PSESP (P26877), LIP_RHIMI (P19515), LIP_RHIOR (P21811), LIP_STAAU (P10335), LIP_STAEP (Q02510), LIP_STAHY (P04635), LIP_THELA (O59952), LIP_VIBCH (P15493),</p> | |

LIPA_PSEFL (P26504), LIPB_PSEFL (P41773), LIPE_AERHY (P40600),
 LIPG_BOVIN (Q29458), LIPG_CANFA (P80035), LIPG_HUMAN (P07098),
 LIPG_RAT (P04634), LIPH_HUMAN (P11150), LIPH_MOUSE (P27656),
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 LIPL_CHICK (P11602), LIPL_FELCA (P55031), LIPL_HUMAN (P06858),
 LIPL_MOUSE (P11152), LIPL_MUSVI (Q46647), LIPL_PAPAN (P49060),
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 LIPP_CAVPO (P50903), LIPP_HORSE (P29183), LIPP_HUMAN (P16233),
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False negative hits (sequences which belong to the set under consideration, but which have not been picked up by the pattern or profile):

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 LIP2_MOUSE (P17892), LIP2_MYOCO (Q64424), LIP3_MORSP (P24640),
 PAFA_CAEEL (Q22943)

'Potential' hits (partial sequences which belong to the set under consideration, but which are not hit by the pattern or profile because they are partial (fragment) sequences):

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Sequences which could potentially belong to the set under consideration:

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 PI7B_ORYSA (Q43360), PIP_BACCO (P46541), RPOB_COXBU (Q87903),
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 YL4K_CAEEL (Q20076), YM23_MYCTU (Q10508), YM24_MYCTU (Q10509),
 YN84_YEAST (P40345), YTXM_BACSU (P23974)


Retrieve an alignment of SWISS-PROT true positive hits:

[Clustal format, color, condensed view] [Clustal format, color] [Clustal format, plain text]
 [Fasta format]

PDB

[Detailed view]

IRP1; 1BU8; 1OIL; 2LIP; 3LIP; 1TAH; 1TGL; 3TGL; 4TGL; 5TGL; 1LGY; 1TIB; 1TIC;
 1HPL; 1LPA; 1LPB; 1ETH; 1TIA;

| | | | | |
|---|-----------------|----------------------|-------------------|----------------|
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PROSITE: PS00120

ID LIPASE_SER; PATTERN.
AC PS00120;
DT APR-1990 (CREATED); NOV-1997 (DATA UPDATE); JUL-1998 (INFO UPDATE).
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DO PDOC00110;
//

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BioRS HTTP API

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AC  PS00120;
DT  APR-1990 (CREATED); NOV-1997 (DATA UPDATE); JUL-1998 (INFO UPDATE).
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DR  P19532, TFE3_HUMAN, F; Q64092, TFE3_MOUSE, F; P08138, TR16_HUMAN, F;
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DR  P43571, YFC5_YEAST, F; P53118, YGO4_YEAST, F; P38796, YHN5_YEAST, F;
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* Lipases, serine active site *

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Triglyceride lipases (EC 3.1.1.3) [1] are lipolytic enzymes that hydrolyzes the ester bond of triglycerides. Lipases are widely distributed in animals, plants and prokaryotes. In higher vertebrates there are at least three tissue-specific isozymes: pancreatic, hepatic, and gastric/lingual. These three types of lipases are closely related to each other as well as to lipoprotein lipase (EC 3.1.1.34) [2], which hydrolyzes triglycerides of chylomicrons and very low density lipoproteins (VLDL).

The most conserved region in all these proteins is centered around a serine residue which has been shown [3] to participate, with an histidine and an aspartic acid residue, to a charge relay system. Such a region is also present in lipases of prokaryotic origin and in lecithin-cholesterol acyltransferase (EC 2.3.1.43) (LCAT) [4], which catalyzes fatty acid transfer between phosphatidylcholine and cholesterol. We have built a pattern from that region.

-Consensus pattern: [LIV]-x-[LIVFY]-[LIVMST]-G-[HYWV]-S-x-G-[GSTAC]
[S is the active site residue]

-Sequences known to belong to this class detected by the pattern: ALL.

-Other sequence(s) detected in Swiss-Prot: 38.

-Note: Drosophila vitellogenins are also related to lipases [5], but they have lost their active site serine.

-Last update: November 1997 / Pattern and text revised.

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- [4] McLean J., Fielding C., Drayna D., Dieplinger H., Baer B., Kohr W.,
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